IN THE SPECIFICATION:

Please amend the specification as follows:

Please replace the second full paragraph on page 5 with the following:

While the above relates to mutants of human serum albumin, it is to be understood that the present invention is not limited to only mutant human serum albumins. Serum albumins across all species display a high degree of conservation and it is well within the expertise of the skilled addressee to identify the amino acids in the positions represented by Xs in the sequence above, from albumins of other species and change said amino acids in order to alter metal binding and/or other physiological characteristic(s). Table 1 in fact shows an alignment of mammalian serum albumin polypeptide sequences in which the residues which may be mutated according to the present invention[[,]] are ~~highlighted~~ denoted by X_n. It is understood that at least one of said residues should be other than the identified native residue in order to generate a mutant serum albumin, which can display altered metal binding and/or other physiological characteristic (s) with respect to the native species serum albumin.

Please replace the caption of Table 1 on page 36 with the following:

Table 1. Comparison of amino acid sequence between mammalian albumins. Residues, which may be mutated are ~~highlighted~~ denoted by X_n. Amino acids before the N terminal amino acid (residue number 1), in the boxed area, are part of the pre-albumin sequence and are cleaved following translation to give albumin itself. Accession numbers of the sequences are Human, P02768; Macaque, M90463; Canine, CAB64867; Feline, P49064; Bovine, P02769; Sheep, P14639; Pig, ABPGS; Rabbit, P49065 and Rat, P02770.